SEQUENCE LISTING

<110> LUKYANOV, SERGI A
SHAGIN, DMITRY A
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10/532,681
<141> 2005-04-26

<160> 22

<170> PatentIn version 3.3

<210> 1
<211> 784
<212> DNA
<213> phialidium sp

<400> 1
gaactgataa aagaaatcat catcatgtct agtggagcac tgttgttcca cggaaagatc 60

ccatatgttg ttgagatgga gggaaatgtt gatggacaca cattctccat tagaggtaaa 120

ggttatggag atgcaagtgt tggtaaagtt gatgcccaat tcatctgcac aactggagat 180

gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc 240

aaatatggtc cagaattaaa ggatttctac aagagttgca tgcctgaagg ctatgtgcag 300

gagcgtacaa tcacatttga aggggacgga gtatttaaaa ctcgcgctga agttacattt 360

gaaaacggat ctgtttataa ccgagtcaaa cttaatggac aaggatttaa gaaagacgga 420

catgtgcttg gaaagaatct tgaattcaat ttcacacctc attgtcttta catttgggga 480

gatcaggcta atcatggttt gaagtctgct ttcaaaatta tgcatgagat tactggatca 540

aaagaagact tcattgttgc agaccacacc caaatgaaca cacccattgg tggtggacca 600

gtccatgtcc ctgaatacca tcatataaca taccatgtca ctctcagcaa agatgttact 660

gatcacaggg ataacatgag cttggttgaa accgtacggg ctgtggattg cagaaaaaca 720

tatctttaaa ttgtaaattt atttgtagtt gaaaaccttt tgtcacgata tataccttta 780

ttat 784

<210> 2
<211> 234
<212> PRT
<213> Phialidium sp

<400> 2

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 3
<211> 705
<212> DNA
<213> Artificial

<220>
<223> phiYFP-Y1 mutant of the phiYFP

<400> 3
atgcctagtg gagcactgtt gttccacgga aagatcccat atgttgttga gatggaggga 60

aatgttgatg gacacacatt ctccattaga ggtaaaggtt atggagatgc aagtgttggt 120

aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240

ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300

gacggagtat ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360

gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa 420

ttcaatttca cacctcattg tctttacatt tggggagatc aggctaatca tggtttgaag 480

tctgctttca aaattatgca tgagattact ggatcaaaag gagacttcat tgttgcagac 540

cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600

atgacatacc atgtcactct cagcaaagat gttactgatc acagggataa catgagcttg 660

gttgaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 4
<211> 234
<212> PRT
<213> Artificial

<220>
<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 5
<211> 705
<212> DNA
<213> Artificial

<220>
<223> phiYFP-M0 mutant of the phiYFP

<400> 5
atgcctagtg gagcactgtt gttccacgga aagatcccat atgttgttga gatggaggga 60

aatgttgatg gacacacatt ctccattaga ggtaaaggtt atggagatgc aagtgttggt 120

aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240

ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300

gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360

gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa 420

ttcaatttca cacctcattg tctttacatt tggggagatc aggctaatca tggtttgaag 480

tctgctttca aaattcgcca tgagattact ggatcaaaag gagacttcat tgttgcagac 540

cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga aaaccatcat 600

atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660

aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 6
<211> 234
<212> PRT
<213> Artificial

<220>
<223> phiYFP-M0 mutant of the phiYFP

<400> 6

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 7
<211> 705
<212> DNA
<213> Artificial

<220>
<223> phiYFP-M1 mutant of the phiYFP

<400> 7
atgtctagtg gagcactgtt gttccacgga aagatcccat atgttgttga gatggaggga 60

aatgttgatg gacacacatt ctccattaga ggtaaaggtt atggagatgc aagtgttggt 120

aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240

ttctacaaga gttgcatgcc tgatggctat gtgcaggagc gtacaatcac atttgaaggg 300

gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360

gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa 420

ttcaatttca cacctcattg tctttacatt tggggagatc aggctaatca tggtttgaag 480

tctgctttca aaatttgcca tgagattact ggatcaaaag gagacttcat tgttgcagac 540

cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600

atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660

aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 8
<211> 234
<212> PRT
<213> Artificial

<220>
<223> phiYFP-M1 mutant of the phiYFP

<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 9
<211> 705
<212> DNA
<213> Artificial

<220>
<223> humanized version of the phiYFP-M1

<400> 9
atgagcagcg gcgccctgct gttccacggc aagatcccct acgtggtgga gatggagggc 60

aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120

aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180

gtgaccaccc tgacctacgg cgcccagtgc ttcgccaagt acggccccga gctgaaggat 240

ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300

gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360

gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420

ttcaatttca ccccccactg cctgtacatc tggggcgatc aggccaatca cggcctgaag 480

agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat 540

cacacccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600

atgagctacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660

aaggagaccg tgcgcgccgt ggattgccgc aagacctacc tgtga 705

<210> 10
<211> 234
<212> PRT
<213> Artificial

<220>
<223> humanized version of the phiYFP-M1

<400> 10

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

```
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
        115                 120                 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130                 135                 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
        195                 200                 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210                 215                 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
```

<210> 11
<211> 1047
<212> DNA
<213> Anthomedusae species

<220>
<221> misc_feature
<223> hydromedusa 1 from sub-order Anthomedusae

<400> 11

```
cttttcttaa aaagaattca aaaaggacgg tttactagac atacttatac agctttactt     60

ataaaggaag aaatgaatgt gatgcgttac aacagaggat tctgcagagt tttgcaaaat    120

ggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaacccgt catacttggt    180

gcaatgacag aaacatttca gaaaaaattg ccatataagt tagaattgga tggagatgtt    240

gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tggtgtaatt    300

gaaggaaaat atgtttgtac agaaggagaa gttcctattt catgggtttc gctcatcacc    360

tcattaagtt atggtgcgaa atgttttgtt cgatatccaa atgaaataaa tgatttttc     420
```

aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgatggt 480

gttttagaaa cagcagctaa aattactatg gaaagtggtg caatagtgaa tagaataaat 540

gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatcctcc 600

cctccttcga caacatatgt tgttcccgag ggagaaggta ttcgaatcat ctatagaaac 660

atctatccaa caaaagatgg tcactatgtt gttgccgaca cacagcaagt aaatcgacca 720

attagagcac aaggaacatc agctatccca acatatcatc acattaaatc gaaagttgat 780

ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca 840

tttgacgctg atttttctta agatttccga tttgcatcaa gattgaaaaa ctaaataaag 900

ataggtaaaa aaaatatgtc tttgatgtta catacagtat tgatataagc ttcaaagaaa 960

tatattttca aataaacttt ataaaattag gaatctttga atatataaac taaacctttt 1020

atttgtagaa taaaaataat taaagac 1047

<210> 12
<211> 262
<212> PRT
<213> Anthomedusae species

<220>
<221> MISC_FEATURE
<223> hydromedusa 1 from sub-order Anthomedusae

<400> 12

Met Asn Val Met Arg Tyr Asn Arg Gly Phe Cys Arg Val Leu Gln Asn
1 5 10 15

Gly Val Lys Asn Leu Arg Ser Arg Asn Cys Ser Thr Glu Glu Lys Pro
20 25 30

Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr
35 40 45

Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile
50 55 60

Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr
65 70 75 80

Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr
85 90 95

Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile
100 105 110

Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg
115 120 125

Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile
130 135 140

```
Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr
145                 150                 155                 160

Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser
                165                 170                 175

Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile
            180                 185                 190

Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala
        195                 200                 205

Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala
    210                 215                 220

Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp
225                 230                 235                 240

Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala
                245                 250                 255

Phe Asp Ala Asp Phe Ser
            260
```

<210> 13
<211> 1089
<212> DNA
<213> Anthomedusae species

<220>
<221> misc_feature
<223> hydromedusa 2 from sub-order Anthomedusae

<400> 13

```
atcattcgct gatacgaagt gaaagtagcg tttgctgaaa gcttcctgga attgctccta     60

cgtatcttga aagttgctcc tacgctccaa cttgtttgtt caaaatggaa ggtggtccag    120

cattatttca atccgatatg acattcaaga tcttcatcga tggagtggtg aatgatcaga    180

aattcacgat aatcgcagat ggatcgtcca aattccccca tggtgacttc aacgtgcatg    240

ctgtgtgcga aaccgggaaa ctcccaatgt catggaaacc tatttgtcac cttatccaat    300

acggggagcc attctttgca aaatatccca atggcatcag ccattttgca caggagtgct    360

ttccagaagg attaacaatt gatcgaacag tcagattcga aaatgacggc actatgacgt    420

ctcaccacac ctatgagttg gacggcacct gtgtcatttc caggataacc gttaattgtg    480

acggatttca acctgatgga ccaatcatga aagaccagct tgttgatatc ctgccaactg    540

agacacatat gttccctcat gggtccaatg ctgtcagaca attgtgctac attggcttca    600

cgacagctga tggtggtctc atgatgtcac attttgattc gaaattgaca ttcaatggtt    660

cgagagcaat caagattcct ggacctcatt tcgttactgt gataatcaaa cagatgaaag    720

atacaagcga caagcgtgat catgtgtgtc aacgtgaagt cacctacgct cactcagttc    780

cacgcatcac ttctgctatc taaacatcat tcttaaaagg ggaacatgca catcatactt    840
```

cagtgtgagg gtcagtgtga gggtctttag atgtcaattt gtcgcaggtg tcacacggcg 900

tcgtttagat gttgaaggac gaaatgcgac aaagagatta atagagactc atatttttat 960

gtagaatcga ttcattcagc ccattggtaa ccttttttggt attttatcat cttattattg 1020

tattggcact ttgtttatat tttgtatgta atgtgtaaac aattgttgaa aatacatgtc 1080

aagaacttg 1089

<210> 14
<211> 232
<212> PRT
<213> Anthomedusae species

<220>
<221> MISC_FEATURE
<223> hydromedusa 2 from sub-order Anthomedusae

<400> 14

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1 5 10 15

Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp
20 25 30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro
130 135 140

Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu
145 150 155 160

Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 15
<211> 699
<212> DNA
<213> Artificial

<220>
<223> S3-2 mutant of hm2CP from a hydromedusa 2 of sub-order Anthomedusa

<400> 15
atggaaggtg gtccagcatt atttcaatcc gacatgacat tcaagatctt catcgatgga 60

gtggtgaatg gtcagaaatt cacgatagtc gcagatggat cgtccaaatt cccccatggt 120

gacttcaacg tacatgctgt gtgcgaaacc gggaaactcc caatgtcatg gaaacccatt 180

tgtcacctta tccaatacgg ggagccattc tttgcaagat atcccaacgg catcagccat 240

tttgcacagg agtgctttcc agaaggatta tcaattgatc gaacagtcag attcgaaaat 300

gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgtttccagg 360

ataaccgtta attgtgacgg atttcaacct gatggaccaa tcatgagaga ccagcttgtt 420

gatatcctgc caaacgagac acatatgttc cctcatggac ccaatgctgt cagacaattg 480

gctttcatag gcttcacgac agctgatggt ggtctcatga tgtcacattt tgattcgaaa 540

atgacattca atggttcgag agcaatcaag attcctggac ctcatttcgt cactaccata 600

accaaacaga tgaaagatac aagcgacaag cgtgatcatg tgtgtcagcg ggaagtcacc 660

tacgctcact cagttccacg catcacttct gctatctaa 699

<210> 16
<211> 232
<212> PRT
<213> Artificial

<220>
<223> S3-2 mutant of hm2CP from a hydromedusa 2 of sub-order Anthomedusae

<400> 16

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1 5 10 15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
20 25 30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 17
<211> 705
<212> DNA
<213> Artificial

<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the phiYFP-M1

<400> 17
atgtccagcg gcgccctgct gttccacggc aagatcccct acgtggtgga gatggagggc 60

aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120

aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180

gtgaccaccc tgtcctacgg cgcccagtgc ttcgccaagt acggccccga gctgaaggat 240

ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300

gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360

gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420

ttcaatttca ccccccactg ccagtacatc tggggcgatc aggccaatca cggcctgaag 480

agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat 540

cacacccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600

atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660

aaggagaccg tgcgcgccgt ggattgccga acagcctacc tgtga 705

<210> 18
<211> 234
<212> PRT
<213> Artificial

<220>
<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

<400> 18

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu
225 230

<210> 19
<211> 705
<212> DNA
<213> Artificial

<220>
<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

<400> 19
atgtccagcg gcgcccagct gttccacggc aagatcccct acgtggtgga gatggagggc 60

aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120

aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180

gtgaccaccc tgtcctgggg cgcccagtgc ttcgccaagt acggccccga gctgaaggat 240

ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300

gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360

gtgaagctga aaggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420

ttcaatttca ccccccacta ccagtacatc tggggcgatc aggccaatca cggcctgaag 480

agcgccttca agatctgcca cgagatcacc ggcagtaagg gcgatttcat cgtggccgat 540

cacacccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600

atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660

aaggagacct tgcgcgccgt ggattgccgc aagacctacc tgtga 705

<210> 20
<211> 234
<212> PRT
<213> Artificial

<220>
<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

<400> 20

Met Ser Ser Gly Ala Gln Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

```
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35                  40                  45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50                  55                  60

Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe
        115                 120                 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130                 135                 140

Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
        195                 200                 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu
    210                 215                 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
```

<210> 21
<211> 699
<212> DNA
<213> Artificial

<220>
<223> humanized version of th S3-2 mutant of hm2cp from a hydromedusa 2 of sub-order Anthomedusae

<400> 21
atggagggcg gccccgccct gttccagagc gacatgacct tcaaaatctt catcgacggc 60

gtggtgaacg gccagaagtt caccatcgtg gccgacggca gcagcaagtt cccccacggc 120

gacttcaacg tgcacgccgt gtgcgagacc ggcaagctgc ccatgagctg gaagcccatc 180

tgccacctga tccagtacgg cgagcccttc ttcgcccgct accccaacgg catcagccac 240

ttcgcccagg agtgcttccc cgagggcctg agcatcgacc gcaccgtgcg cttcgagaac 300

gacggcacca tgaccagcca ccacacctac gagctggacg gcacctgcgt ggtgagccgc 360

atcaccgtga actgcgacgg cttccagccc gacggcccca tcatgcgcga ccagctggtg 420

gacatcctgc ccaacgagac ccacatgttc ccccacggcc ccaacgccgt gcgccagctg 480

gccttcatcg gcttcaccac cgccgacggc ggcctgatga tgagccactt cgacagcaag 540

atgaccttca acggcagccg cgccatcaag atccccggcc cccacttcgt gaccaccatc 600

accaagcaga tgaaggacac cagcgacaag cgcgaccacg tgtgccagcg cgaggtgacc 660

tacgcccaca gcgtgccccg catcaccagc gccatctga 699

<210> 22
<211> 232
<212> PRT
<213> Artificial

<220>
<223> humanized S3-2 mutant of hm2cp from a hydromedusa 2 of sub-order Anthomedusae

<400> 22

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1 5 10 15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
20 25 30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230